



SEQUENCE LISTING

<110> Nielsen, Bjarne R.
Nielsen, Ruby
Lehmbeck, Jan

<120> Thermostable Glucoamylase

<130> 5279.210-US

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 25

<212> PRT

<213> Talaromyces emersonii

<220>

<221> misc_feature

<223> Xaa at position 13 denotes a residue that could
not be assigned

<400> 1

Ala Asn Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Xaa Pro Ile Ala
1 5 10 15

Leu Gln Gly Val Leu Asn Asn Ile Gly
20 25

<210> 2

<211> 20

<212> PRT

<213> Talaromyces emersonii

<400> 2

Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser Thr Gly Gly Leu
1 5 10 15

Gly Glu Pro Lys
20

<210> 3

<211> 22

<212> PRT

<213> Talaromyces emersonii

<220>

<221> misc_feature
 <222> (0)..(22)
 <223> Xaa denotes a residue that could not be assigned

<400> 3

Xaa Asn Val Asn Glu Thr Ala Phe Thr Gly Pro Xaa Gly Arg Pro Gln
 1 5 10 15

Arg Asp Gly Pro Ala Leu
 20

<210> 4
 <211> 35
 <212> PRT
 <213> Talaromyces emersonii

<400> 4

Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly
 1 5 10 15

Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala
 20 25 30

Asn His Lys
 35

<210> 5
 <211> 16
 <212> PRT
 <213> Talaromyces emersonii

<220>
 <221> misc_feature
 <222> (0)..(16)
 <223> Xaa denotes a residue that could not be assigned

<400> 5

Thr Xaa Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys
 1 5 10 15

<210> 6
 <211> 35
 <212> PRT
 <213> Talaromyces emersonii

<400> 6

Ala Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
 1 5 10 15

Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu Asp Asp
 20 25 30

Ser Trp Gln
 35

<210> 7
 <211> 591
 <212> PRT
 <213> Talaromyces emersonii

<400> 7

Ala Thr Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala
 1 5 10 15

Leu Gln Gly Val Leu Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala
 20 25 30

Gly Ala Ser Ala Gly Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro
 35 40 45

Asn Tyr Phe Tyr Ser Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr
 50 55 60

Leu Val Asp Ala Phe Asn Arg Gly Asn Lys Asp Leu Glu Gln Thr Ile
 65 70 75 80

Gln Gln Tyr Ile Ser Ala Gln Ala Lys Val Gln Thr Ile Ser Asn Pro
 85 90 95

Ser Gly Asp Leu Ser Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn Val
 100 105 110

Asn Glu Thr Ala Phe Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly
 115 120 125

Pro Ala Leu Arg Ala Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile
 130 135 140

Asp Asn Gly Glu Ala Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val
 145 150 155 160

Gln Asn Asp Leu Ser Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe
165 170 175

Asp Leu Trp Glu Glu Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val
180 185 190

Gln His Arg Ala Leu Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn
195 200 205

His Thr Cys Ser Asn Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe
210 215 220

Leu Gln Ser Tyr Trp Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly
225 230 235 240

Ser Gly Arg Ser Gly Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His
245 250 255

Thr Phe Asp Pro Ala Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys
260 265 270

Ser Ala Arg Ala Leu Ala Asn His Lys Val Val Thr Asp Ser Phe Arg
275 280 285

Ser Ile Tyr Ala Ile Asn Ser Gly Ile Ala Glu Gly Ser Ala Val Ala
290 295 300

Val Gly Arg Tyr Pro Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr
305 310 315 320

Leu Ala Thr Ala Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln
325 330 335

Trp Lys Lys Ile Gly Ser Ile Ser Ile Thr Asp Val Ser Leu Pro Phe
340 345 350

Phe Gln Asp Ile Tyr Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly
355 360 365

Ser Thr Thr Phe Asn Asp Ile Ile Ser Ala Val Gln Thr Tyr Gly Asp
370 375 380

Gly Tyr Leu Ser Ile Val Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu
 385 390 395 400

Thr Glu Gln Phe Ser Arg Thr Asp Gly Thr Pro Leu Ser Ala Ser Ala
 405 410 415

Leu Thr Trp Ser Tyr Ala Ser Leu Leu Thr Ala Ser Ala Arg Arg Gln
 420 425 430

Ser Val Val Pro Ala Ser Trp Gly Glu Ser Ser Ala Ser Ser Val Leu
 435 440 445

Ala Val Cys Ser Ala Thr Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr
 450 455 460

Asn Thr Val Trp Pro Ser Ser Gly Ser Gly Ser Ser Thr Thr Thr Ser
 465 470 475 480

Ser Ala Pro Cys Thr Thr Pro Thr Ser Val Ala Val Thr Phe Asp Glu
 485 490 495

Ile Val Ser Thr Ser Tyr Gly Glu Thr Ile Tyr Leu Ala Gly Ser Ile
 500 505 510

Pro Glu Leu Gly Asn Trp Ser Thr Ala Ser Ala Ile Pro Leu Arg Ala
 515 520 525

Asp Ala Tyr Thr Asn Ser Asn Pro Leu Trp Tyr Val Thr Val Asn Leu
 530 535 540

Pro Pro Gly Thr Ser Phe Glu Tyr Lys Phe Phe Lys Asn Gln Thr Asp
 545 550 555 560

Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro
 565 570 575

Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu Asp Asp Ser Trp Gln
 580 585 590

<210> 8
 <211> 1605
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> CDS
 <222> (1)..(1602)

<220>
 <221> sig_peptide
 <222> (1)..(72)

<220>
 <221> mat_peptide
 <222> (73)..()

<400> 8
 atg tcg ttc cga tct cta ctc gcc ctg agc ggc ctc gtc tgc aca ggg 48
 Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 -20 -15 -10

ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc 96
 Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
 -5 -1 1 5

aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg 144
 Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
 10 15 20

gac ggt gct tgg gtg tcg ggc gcg gac tct ggc att gtc gtt gct agt 192
 Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
 25 30 35 40

ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct 240
 Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
 45 50 55

ggt ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc 288
 Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
 60 65 70

agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc 336
 Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
 75 80 85

cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc 384
 Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
 90 95 100

ggt gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg 432
 Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
 105 110 115 120

gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc 480
 Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
 125 130 135

ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg 528
 Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr

140	145	150	
gac att gtt tgg ccc ctc gtt agg aac gac ctg tcg tat gtg gct caa Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln 155 160 165			576
tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tcg Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser 170 175 180			624
tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser 185 190 195 200			672
gcc ttc gcg acg gcc gtc ggc tcg tcc tgc tcc tgg tgt gat tct cag Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln 205 210 215			720
gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe 220 225 230			768
att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr 235 240 245			816
ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp 250 255 260			864
tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu 265 270 275 280			912
gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser 285 290 295			960
gac agc gag gct gtt gcg gtg ggt cgg tac cct gag gac acg tac tac Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr 300 305 310			1008
aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Glu Gln Leu 315 320 325			1056
tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr 330 335 340			1104
gat gtg tcg ctg gac ttc ttc aag gca ctg tac agc gat gct gct act Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr 345 350 355 360			1152
ggc acc tac tct tcg tcc agt tcg act tat agt agc att gta gat gcc Gly Thr Tyr Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala 365 370 375			1200

gtg aag act ttc gcc gat ggc ttc gtc tct att gtg gaa act cac gcc Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala 380 385 390	1248
gca agc aac ggc tcc atg tcc gag caa tac gac aag tct gat ggc gag Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu 395 400 405	1296
cag ctt tcc gct cgc gac ctg acc tgg tct tat gct gct ctg ctg acc Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr 410 415 420	1344
gcc aac aac cgt cgt aac tcc gtc gtg cct gct tct tgg ggc gag acc Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr 425 430 435 440	1392
tct gcc agc agc gtg ccc ggc acc tgt gcg gcc aca tct gcc att ggt Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly 445 450 455	1440
acc tac agc agt gtg act gtc acc tcg tgg ccg agt atc gtg gct act Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr 460 465 470	1488
ggc ggc acc act acg acg gct acc ccc act gga tcc ggc agc gtg acc Gly Gly Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr 475 480 485	1536
tcg acc agc aag acc acc gcg act gct agc aag acc agc acc acg acc Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr 490 495 500	1584
cgc tct ggt atg tca ctg tga Arg Ser Gly Met Ser Leu 505 510	1605

<210> 9
 <211> 534
 <212> PRT
 <213> Aspergillus niger

<400> 9

Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly -20 -15 -10
--

Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser -5 -1 1 5
--

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala 10 15 20

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
 25 30 35 40

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
 45 50 55

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
 60 65 70

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
 75 80 85

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
 90 95 100

Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
 105 110 115 120

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
 125 130 135

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
 140 145 150

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
 155 160 165

Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
 170 175 180

Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
 185 190 195 200

Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
 205 210 215

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
 220 225 230

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
 235 240 245

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp

250		255		260
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu				
265		270		275
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser				
	285		290	295
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr				
	300		305	310
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu				
	315		320	325
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr				
	330		335	340
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr				
	345		350	355
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala				
	365		370	375
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala				
	380		385	390
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu				
	395		400	405
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr				
	410		415	420
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr				
	425		430	435
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly				
	445		450	455
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr				
	460		465	470
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr				
	475		480	485

Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
 490 495 500

Arg Ser Gly Met Ser Leu
 505 510

<210> 10
 <211> 534
 <212> PRT
 <213> Aspergillus niger

<220>
 <221> SIGNAL
 <222> (1)..(24)

<400> 10

Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1 5 10 15

Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
 20 25 30

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
 35 40 45

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
 50 55 60

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
 65 70 75 80

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
 85 90 95

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
 100 105 110

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
 115 120 125

Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
 130 135 140

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
 145 150 155 160

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
 165 170 175

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
 180 185 190

Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
 195 200 205

Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
 210 215 220

Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
 225 230 235 240

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
 245 250 255

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
 260 265 270

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
 275 280 285

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
 290 295 300

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
 305 310 315 320

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
 325 330 335

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
 340 345 350

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
 355 360 365

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
 370 375 380

Gly Thr Tyr Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
 385 390 395 400

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
 405 410 415

Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
 420 425 430

Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
 435 440 445

Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
 450 455 460

Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
 465 470 475 480

Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
 485 490 495

Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
 500 505 510

Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
 515 520 525

Arg Ser Gly Met Ser Leu
 530

<210> 11
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <223> N in position 3 = A, G, C, T

<400> 11
gtnttraaya ayathgg 17

<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<223> N= A, G, C, T

<400> 12
gtnctnaaya ayathgg 17

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<223> N= A, G, C, T

<400> 13
ctr ganaccc tyctyca 17

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
ctraayaccc tyctyca 17

<210> 15
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
 <221> misc_feature
 <223> N= A, G, C, T

 <400> 15
 accctyctrc trggntt 17

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 16
 gtgagcccaa gttcaatgtg 20

 <210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 17
 agaaatcggg tatcctttca g 21

 <210> 18
 <211> 105
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 18
 gctcctcatg gtggatcccc agttgtgtat atagaggatt gaggaaggaa gagaagtgtg 60
 gatagaggtg aattgagttg gaaactccaa gcatggcatc cttgc 105

 <210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 19

gacagatctc caccatggcg tccctcggtg 30

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
gacctcgagt cactgccaac tatcgtc 27

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ccctcaccag gggaatgctg cagttgatg 29

<210> 22
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
cgccattctc ggcgactt 18

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
cgccgcggta ttctgcag 18

<210> 24
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 24
caatataaac gacggtaccc gggagatctc caccatggcg tccctcgttg 50

<210> 25
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
ctaattacat catgcggccc tctagatcac tgccaactat cgtc 44

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
aatttggtc gctcctgctc g 21

<210> 27
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 27
cgagcaggag cgacccaaat tatttctact cctggacacg 40

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 28
gatgagatag ttgcatacg 20

<210> 29
<211> 43
<212> DNA

<213> Artificial Sequence
 <220>
 <223> Primer
 <400> 29
 cgtatgcgaa ctatctcatc gacaacggcg aggcttcgac tgc 43
 <210> 30
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 30
 cgaaggtgga tgagttccag 20
 <210> 31
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 31
 ctggaactca tccaccttcg acctctggga agaagtagaa gg 42
 <210> 32
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 32
 gacaatactc agatatccat c 21
 <210> 33
 <211> 43
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 33
 gatggatatc tgagtattgt cgagaaatat actccctcag acg 43

<210> 34
 <211> 2748
 <212> DNA
 <213> *Talaromyces emersonii*

<400> 34
 acgagatgtg tatatactgt gaaccaaact agatgatgtc agttatgctg gtctgagaac 60
 tcatagaagc ccttgaaaat accccaagct agcactccaa ccctaactct gttgctctac 120
 tagatcaaga cgagtactct gattgagctg caggcttgga atatatgatt agcagaaaaa 180
 ggggttaaaac ttgtatgaca atcagtttgt cagtactccg tagtgatgcc atgtctatag 240
 agtcgacact aaggcagcat gtgaatgagt cggaaatgac aggaagcaga ttccttaaca 300
 gtcattgttct ccgtgcctgc atccccacgt cacctgcaaa gatgcgacgc tactccacac 360
 cggcgccttg atgtctgctg ttcctggcct agtggagccc catgcgctgc tagctcgtgg 420
 tcttcgaata aatcagaata aaaaacggag taattaattg cgcccgcaac aaactaagca 480
 atgtaactca atgccaagct tccgctgatg ctcttgacat ctccgtagtg gcttctttcg 540
 taatttcaga cgtatatata gtagtaatgc ccagcaggcc gggataatga tggggatttc 600
 tgaactctca gcttccgtac gctgaacagt ttgcttgctg tgtcaaccat ggcgtccctc 660
 gttgctggcg ctctctgcat cctgggcctg acgcctgctg catttgacag agcgcccgtt 720
 gcagcgcgag ccaccggttc cctggactcc tttctcgcaa ccgaaactcc aattgccctc 780
 caaggcgtgc tgaacaacat cgggcccaat ggtgctgatg tggcaggagc aagcgccggc 840
 attgtggttg ccagtccgag caggagcgac ccaaattgta ggttctttcc caccagaaat 900
 tacttattta aatcagccct ctgacagggt gaagatttct actcctggac acgtgacgca 960
 gcgctcacgg ccaaatacct cgtcgacgcc ttcacgcgg gcaacaagga cctagagcag 1020
 accatccagc agtacatcag cgcgcaggcg aagggtgcaa ctatctccaa tccgtccgga 1080
 gatttatcca ccggtggctt aggtgagccc aagttcaatg tgaatgagac ggcttttacc 1140
 gggccctggg gtcgtccaca gagggacgga ccagcggtga gagcgacggc cctcattgcg 1200
 tatgcgaact atctcatcgt aagcttctgc tcgctgccct tctctctgct cgtatgctaa 1260
 gtagtcctgt caggacaacg gcgaggcttc gactgccgat gagatcatct ggccgattgt 1320
 ccagaatgat ctgtcctaca tcaccaata ctggaactca tccaccttcg gtaggcaaat 1380
 gaatattccc gacacagcgt ggtactaatt tgattcagac ctctgggaag aagtagaagg 1440
 atcctcattc ttcacaaccg ccgtgcaaca ccgcgccctg gtcgaaggca atgcactggc 1500
 aacaaggctg aaccacacgt gctccaactg cgtctctcag gccccctcagg tcctgtgttt 1560

cctgcagtca tactggaccg gatcgtatgt tctggccaac tttggtggca gcggtcgttc 1620
cggcaaggac gtgaattcga ttctgggcag catccacacc tttgatcccg ccggaggctg 1680
tgacgactcg accttccagc cgtgttcggc ccgtgccttg gcaaatacaca aggtgggtcac 1740
cgactcgttc cggagtatct atgcgatcaa ctcaggcatc gcagagggat ctgccgtggc 1800
agtcggccgc taccctgagg atgtctacca gggcgggaac ccctggtacc tggccacagc 1860
agcggctgca gagcagcttt acgacgccat ctaccagtgg aagaagatcg gctcgataag 1920
tatcacggac gttagtctgc cttttttcca ggatatctac ctttctgccg cgggtgggcac 1980
ctataactct ggctccacga ctttcaacga catcatctcg gccgtccaga cgtatggtga 2040
tggatatctg agtattgtcg tacgttttgc cttagattct caggtgtaaa gaaaaaatg 2100
gaactaactc agttctagga gaaatatact ccctcagacg gctctcttac cgaacaattc 2160
tcccgtacag acggcactcc gctttctgcc tctgccctga cttggtcgta cgcttctctc 2220
ctaaccgctt cggcccgag acagtcgctc gtccctgctt cctggggcga aagctccgca 2280
agcagcgtcc ctgccgtctg ctctgccacc tctgccacgg gcccatacag cacggctacc 2340
aacaccgtct ggccaagctc tggctctggc agctcaacaa ccaccagtag cgcccatgc 2400
accactccta cctctgtggc tgtgacctc gacgaaatcg tcagcaccag ttacggggag 2460
acaatctacc tggccggctc gatccccgag ctgggcaact ggtccacggc cagcgcgatc 2520
cccctccgcg cggatgctta caccaacagc aaccgctctt ggtacgtgac cgtcaatctg 2580
ccccctggca ccagcttcga gtacaagttc ttcaagaacc agacggacgg gaccatcgtc 2640
tgggaagacg acccgaaccg gtcgtacacg gtcccagcgt actgtgggca gactaccgcc 2700
attcttgacg atagttggca gtgagataac atccaccctt ctgtttta 2748

<210> 35
<211> 618
<212> PRT
<213> Talaromyces emersonii

<400> 35

Met Ala Ser Leu Val Ala Gly Ala Leu Cys Ile Leu Gly Leu Thr Pro
1 5 10 15

Ala Ala Phe Ala Arg Ala Pro Val Ala Ala Arg Ala Thr Gly Ser Leu
20 25 30

Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala Leu Gln Gly Val Leu
 35 40 45

Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala Gly Ala Ser Ala Gly
 50 55 60

Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro Asn Tyr Phe Tyr Ser
 65 70 75 80

Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe
 85 90 95

Ile Ala Gly Asn Lys Asp Leu Glu Gln Thr Ile Gln Gln Tyr Ile Ser
 100 105 110

Ala Gln Ala Lys Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser
 115 120 125

Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn Val Asn Glu Thr Ala Phe
 130 135 140

Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala
 145 150 155 160

Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile Asp Asn Gly Glu Ala
 165 170 175

Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser
 180 185 190

Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe Asp Leu Trp Glu Glu
 195 200 205

Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu
 210 215 220

Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn His Thr Cys Ser Asn
 225 230 235 240

Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe Leu Gln Ser Tyr Trp
 245 250 255

Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly

260	265	270
Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala		
275	280	285
Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu		
290	295	300
Ala Asn His Lys Val Val Thr Asp Ser Phe Arg Ser Ile Tyr Ala Ile		
305	310	315
Asn Ser Gly Ile Ala Glu Gly Ser Ala Val Ala Val Gly Arg Tyr Pro		
325	330	335
Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala		
340	345	350
Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys Lys Ile Gly		
355	360	365
Ser Ile Ser Ile Thr Asp Val Ser Leu Pro Phe Phe Gln Asp Ile Tyr		
370	375	380
Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly Ser Thr Thr Phe Asn		
385	390	395
Asp Ile Ile Ser Ala Val Gln Thr Tyr Gly Asp Gly Tyr Leu Ser Ile		
405	410	415
Val Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser		
420	425	430
Arg Thr Asp Gly Thr Pro Leu Ser Ala Ser Ala Leu Thr Trp Ser Tyr		
435	440	445
Ala Ser Leu Leu Thr Ala Ser Ala Arg Arg Gln Ser Val Val Pro Ala		
450	455	460
Ser Trp Gly Glu Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala		
465	470	475
Thr Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr Asn Thr Val Trp Pro		
485	490	495

Ser Ser Gly Ser Gly Ser Ser Thr Thr Thr Ser Ser Ala Pro Cys Thr
500 505 510

Thr Pro Thr Ser Val Ala Val Thr Phe Asp Glu Ile Val Ser Thr Ser
515 520 525

Tyr Gly Glu Thr Ile Tyr Leu Ala Gly Ser Ile Pro Glu Leu Gly Asn
530 535 540

Trp Ser Thr Ala Ser Ala Ile Pro Leu Arg Ala Asp Ala Tyr Thr Asn
545 550 555 560

Ser Asn Pro Leu Trp Tyr Val Thr Val Asn Leu Pro Pro Gly Thr Ser
565 570 575

Phe Glu Tyr Lys Phe Phe Lys Asn Gln Thr Asp Gly Thr Ile Val Trp
580 585 590

Glu Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala Tyr Cys Gly Gln
595 600 605

Thr Thr Ala Ile Leu Asp Asp Ser Trp Gln
610 615